

M. Mouslipour

1652

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OIPE

#17
DMT
10-9-01

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/369,735B

DATE: 07/23/2001

TIME: 16:02:39

Input Set : A:\11059 002001.TXT

Output Set: N:\CRF3\07232001\I369735B.raw

ENTERED

4 <110> APPLICANT: Matsui, Ikuo
5 Ishikawa, Kazuhiko
6 Ishida, Hiroyasu
7 Kosugi, Yoshitsugu
9 <120> TITLE OF INVENTION: THERMOPHILIC ENZYMES HAVING
10 BETA-GLYCOSIDASE ACTIVITY
12 <130> FILE REFERENCE: 11059/002001
14 <140> CURRENT APPLICATION NUMBER: 09/369,735B
15 <141> CURRENT FILING DATE: 1999-08-06
17 <160> NUMBER OF SEQ ID NOS: 10
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1269
23 <212> TYPE: DNA
24 <213> ORGANISM: Pyrococcus horikoshii
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)...(1269)
30 <400> SEQUENCE: 1
31 atg ccg ctg aaa ttc ccg gaa atg ttt ctc ttt ggt acc gca aca tca 48
32 Met Pro Leu Lys Phe Pro Glu Met Phe Leu Phe Gly Thr Ala Thr Ser
33 1 5 10 15
35 tcc cat cag ata gag gga aat aat aga tgg aat gat tgg tgg tac tat 96
36 Ser His Gln Ile Glu Gly Asn Asn Arg Trp Asn Asp Trp Trp Tyr Tyr
37 20 25 30
39 gag cag att gga aag ctc ccc tac aga tct ggt aag gct tgc aat cac 144
40 Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His
41 35 40 45
43 tgg gaa ctt tac agg gat gat att cag cta atg acc agc ttg ggc tat 192
44 Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr
45 50 55 60
47 aat gct tat agg ttc tcc ata gag tgg agc agg cta ttc cca gag gaa 240
48 Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu
49 65 70 75 80
51 aat aaa ttt aat gaa gat gct ttc atg aaa tac cgg gag att ata gac 288
52 Asn Lys Phe Asn Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp
53 85 90 95
55 ttg tta ttg acg aga ggt ata act ccc ctg gtg acc cta cac cac ttt 336
56 Leu Leu Leu Thr Arg Gly Ile Thr Pro Leu Val Thr Leu His His Phe
57 100 105 110
59 act agc cct ctc tgg ttc atg aag aaa ggt ggc ttc ctt agg gag gag 384
60 Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu
61 115 120 125
63 aac cta aaa cat tgg gaa aag tac ata gaa aag gtt gct gag ctt tta 432
64 Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu
65 130 135 140
67 gaa aaa gtt aaa cta gta gct acc ttc aat gag ccg atg gta tac gta 480

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68	Glu	Lys	Val	Lys	Leu	Val	Ala	Thr	Phe	Asn	Glu	Pro	Met	Val	Tyr	Val	
69	145				150					155						160	
71	atg	atg	gga	tat	cta	acg	gct	tat	tgg	ccc	cca	ttc	att	agg	agt	cca	528
72	Met	Met	Gly	Tyr	Leu	Thr	Ala	Tyr	Trp	Pro	Pro	Phe	Ile	Arg	Ser	Pro	
73					165					170						175	
75	ttt	aag	gcc	ttt	aag	gta	gct	gca	aac	ctg	ctt	aaa	gct	cac	gca	att	576
76	Phe	Lys	Ala	Phe	Lys	Val	Ala	Ala	Asn	Leu	Leu	Lys	Ala	His	Ala	Ile	
77					180					185						190	
79	gcc	tat	gaa	ctt	ctt	cat	ggg	aaa	ttc	aaa	gtt	gga	atc	gta	aag	aat	624
80	Ala	Tyr	Glu	Leu	Leu	His	Gly	Lys	Phe	Lys	Val	Gly	Ile	Val	Lys	Asn	
81					195					200						205	
83	att	ccc	ata	ata	ctc	cca	gcg	agt	gac	aag	gag	agg	gat	aga	aaa	gcc	672
84	Ile	Pro	Ile	Ile	Leu	Pro	Ala	Ser	Asp	Lys	Glu	Arg	Asp	Arg	Lys	Ala	
85					210					215						220	
87	gct	gag	aaa	gct	gat	aat	tta	ttt	aac	tgg	cac	ttt	ttg	gat	gcg	ata	720
88	Ala	Glu	Lys	Ala	Asp	Asn	Leu	Phe	Asn	Trp	His	Phe	Leu	Asp	Ala	Ile	
89	225					230					235					240	
91	tgg	agt	ggg	aaa	tac	aga	ggg	gta	ttt	aaa	aca	tat	agg	att	ccc	caa	768
92	Trp	Ser	Gly	Lys	Tyr	Arg	Gly	Val	Phe	Lys	Thr	Tyr	Arg	Ile	Pro	Gln	
93					245					250						255	
95	agt	gac	gca	gat	ttc	att	ggg	gtt	aac	tat	tac	acg	gcc	agc	gaa	gta	816
96	Ser	Asp	Ala	Asp	Phe	Ile	Gly	Val	Asn	Tyr	Tyr	Thr	Ala	Ser	Glu	Val	
97					260					265						270	
99	agg	cat	act	tgg	aat	cct	tta	aaa	ttc	ttc	ttt	gag	gtg	aaa	tta	gcg	864
100	Arg	His	Thr	Trp	Asn	Pro	Leu	Lys	Phe	Phe	Phe	Glu	Val	Lys	Leu	Ala	
101					275					280						285	
103	gat	att	agc	gag	agg	aag	act	caa	atg	gga	tgg	agc	gtt	tat	cca	aaa	912
104	Asp	Ile	Ser	Glu	Arg	Lys	Thr	Gln	Met	Gly	Trp	Ser	Val	Tyr	Pro	Lys	
105					290					295						300	
107	gga	ata	tac	atg	gcc	ctt	aaa	aaa	gct	tcc	agg	tat	gga	agg	cct	ctt	960
108	Gly	Ile	Tyr	Met	Ala	Leu	Lys	Lys	Ala	Ser	Arg	Tyr	Gly	Arg	Pro	Leu	
109	305					310					315					320	
111	tat	att	acg	gaa	aac	gga	ata	gcg	acg	ctt	gat	gat	gaa	tgg	aga	gtg	1008
112	Tyr	Ile	Thr	Glu	Asn	Gly	Ile	Ala	Thr	Leu	Asp	Asp	Glu	Trp	Arg	Val	
113					325					330						335	
115	gaa	ttc	ata	att	caa	cac	ctc	caa	tac	gtt	cat	aag	gct	atc	gaa	gac	1056
116	Glu	Phe	Ile	Ile	Gln	His	Leu	Gln	Tyr	Val	His	Lys	Ala	Ile	Glu	Asp	
117					340					345						350	
119	ggc	ctg	gat	gta	aga	ggt	tac	ttc	tat	tgg	tca	ttt	atg	gat	aac	tac	1104
120	Gly	Leu	Asp	Val	Arg	Gly	Tyr	Phe	Tyr	Trp	Ser	Phe	Met	Asp	Asn	Tyr	
121					355					360						365	
123	gag	tgg	aaa	gag	ggg	ttt	ggg	cct	aga	ttt	ggc	cta	gtg	gaa	gtt	gat	1152
124	Glu	Trp	Lys	Glu	Gly	Phe	Gly	Pro	Arg	Phe	Gly	Leu	Val	Glu	Val	Asp	
125					370					375						380	
127	tat	caa	acc	ttc	gag	aga	agg	ccc	agg	aag	agt	gct	tac	gta	tac	gga	1200
128	Tyr	Gln	Thr	Phe	Glu	Arg	Arg	Pro	Arg	Lys	Ser	Ala	Tyr	Val	Tyr	Gly	
129	385					390					395					400	
131	gaa	att	gca	aga	agt	aag	gaa	ata	aag	gat	gag	cta	tta	aag	aga	tat	1248
132	Glu	Ile	Ala	Arg	Ser	Lys	Glu	Ile	Lys	Asp	Glu	Leu	Leu	Lys	Arg	Tyr	

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file://C:\CRF3\Outhold\VsrI369735B.htm

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186 Tyr Ile Thr Glu Asn Gly Ile Ala Thr Leu Asp Asp Glu Trp Arg Val
187 325 330 335
188 Glu Phe Ile Ile Gln His Leu Gln Tyr Val His Lys Ala Ile Glu Asp
189 340 345 350
190 Gly Leu Asp Val Arg Gly Tyr Phe Tyr Trp Ser Phe Met Asp Asn Tyr
191 355 360 365
192 Glu Trp Lys Glu Gly Phe Gly Pro Arg Phe Gly Leu Val Glu Val Asp
193 370 375 380
194 Tyr Gln Thr Phe Glu Arg Arg Pro Arg Lys Ser Ala Tyr Val Tyr Gly
195 385 390 395 400
196 Glu Ile Ala Arg Ser Lys Glu Ile Lys Asp Glu Leu Leu Lys Arg Tyr
197 405 410 415
198 Gly Leu Pro Glu Leu Gln Leu
199 420
201 <210> SEQ ID NO: 3
202 <211> LENGTH: 57
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence ✓
206 <220> FEATURE:
207 <223> OTHER INFORMATION: An upper primer designed to create the NdeI site. ✓
209 <400> SEQUENCE: 3
210 taagaaggag atatacatat gccgctgaaa ttcccggaaa tgtttctctt tggtagc 57
212 <210> SEQ ID NO: 4
213 <211> LENGTH: 46
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence ✓
217 <220> FEATURE:
218 <223> OTHER INFORMATION: A lower primer designed to create the BamHI site. ✓
220 <400> SEQUENCE: 4
221 tttactgcag agaggatccc taatcctaaa gttgaagttc tggtag 46
223 <210> SEQ ID NO: 5
224 <211> LENGTH: 423
225 <212> TYPE: PRT
226 <213> ORGANISM: Pyrococcus horikoshii
228 <400> SEQUENCE: 5
229 Met Pro Leu Lys Phe Pro Glu Met Phe Leu Phe Gly Thr Ala Thr Ser
230 1 5 10 15
231 Ser Lys Cys Ile Glu Gly Asn Asn Arg Trp Asn Cys Trp Trp Tyr Tyr
232 20 25 30
233 Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His
234 35 40 45
235 Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr
236 50 55 60
237 Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu
238 65 70 75 80
239 Asn Lys Phe Met Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp
240 85 90 95
241 Leu Leu Leu Thr Phe Gly Ile Thr Pro Leu Val Thr Leu His His Phe
242 100 105 110

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243 Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu
244      115      120      125
245 Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu
246      130      135      140
247 Glu Lys Val Lys Leu Val Ala Thr Phe Asn Glu Pro Met Val Tyr Val
248 145      150      155      160
249 Met Met Gly Tyr Leu Thr Ala Tyr Trp Pro Pro Phe Ile Arg Ser Pro
250      165      170      175
251 Phe Lys Ala Phe Lys Val Ala Ala Asn Leu Leu Lys Ala His Ala Ile
252      180      185      190
253 Ala Tyr Glu Leu Leu His Gly Lys Phe Lys Val Gly Ile Val Lys Asn
254      195      200      205
255 Ile Pro Ile Ile Leu Pro Ala Ser Asp Lys Glu Arg Asp Arg Lys Ala
256      210      215      220
257 Ala Glu Lys Ala Asp Asn Leu Phe Asn Trp His Phe Leu Asp Ala Ile
258 225      230      235      240
259 Trp Ser Gly Lys Tyr Arg Gly Val Phe Lys Thr Tyr Arg Ile Pro Gln
260      245      250      255
261 Ser Asp Ala Asp Phe Ile Gly Met Asn Tyr Tyr Thr Ala Ser Glu Val
262      260      265      270
263 Arg His Thr Trp Asn Pro Leu Lys Phe Phe Phe Glu Val Lys Leu Ala
264      275      280      285
265 Asp Ile Ser Glu Arg Lys Thr Gln Met Gly Trp Ser Val Tyr Pro Lys
266      290      295      300
267 Gly Ile Tyr Met Ala Leu Lys Lys Ala Ser Pro Tyr Gly Arg Pro Leu
268 305      310      315      320
269 Tyr Ile Thr Glu Asn Gly Ile Ala Thr Leu Asp Asp Glu Trp Arg Val
270      325      330      335
271 Glu Phe Ile Ile Gln His Leu Gln Tyr Val His Lys Ala Ile Glu Asp
272      340      345      350
273 Gly Leu Asp Val Arg Gly Tyr Phe Tyr Trp Ser Phe Met Asp Asn Tyr
274      355      360      365
275 Glu Trp Lys Glu Gly Phe Gly Pro Arg Phe Gly Leu Val Glu Val Asp
276      370      375      380
277 Tyr Gln Thr Phe Glu Arg Arg Pro Arg Lys Ser Ala Tyr Val Tyr Gly
278 385      390      395      400
279 Glu Ile Ala Arg Ser Lys Glu Ile Lys Asp Glu Leu Leu Lys Arg Tyr
280      405      410      415
281 Gly Leu Pro Glu Leu Gln Leu
282      420
284 <210> SEQ ID NO: 6
285 <211> LENGTH: 483
286 <212> TYPE: PRT
287 <213> ORGANISM: Pyrococcus horikoshii
289 <400> SEQUENCE: 6
290 Met Lys Phe Tyr Trp Gly Val Val Gln Ser Ala Phe Gln Phe Glu Met
291 1      5      10      15
292 Gly Asp Pro Tyr Arg Arg Asn Ile Asp Pro Arg Ser Asp Trp Trp Tyr
293      20      25      30
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VERIFICATION SUMMARY

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Input Set : A:\11059 002001.TXT

Output Set: N:\CRF3\07232001\I369735B.raw